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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/662,812

DATE: 05/09/2002

TIME: 13:44:41

Input Set : A:\seqed.app.txt

Output Set: N:\CRF3\05092002\I662812.raw

3 <110> APPLICANT: Andrew D. MURDIN, Raymond P. OOMEN, Joe WANG, Pamela DUNN
5 <120> TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses
thereof
7 <130> FILE REFERENCE: 77813-27
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/662,812
C--> 10 <141> CURRENT FILING DATE: 2000-09-15
12 <150> PRIOR APPLICATION NUMBER: US 60/154,652
13 <151> PRIOR FILING DATE: 1999-09-20
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1907
21 <212> TYPE: DNA
22 <213> ORGANISM: Chlamydia pneumoniae
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (101)..(1804)
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31 aaacattgaa atacttgcta gaggagttga acatcgatct atg gga cta ttc cat 115
32 Met Gly Leu Phe His
33 1 5
35 cta act ctc ttt gga ctt tta ttg tgt agt ctt ccc att tct ctt gtt 163
36 Leu Thr Leu Phe Gly Leu Leu Leu Cys Ser Leu Pro Ile Ser Leu Val
37 10 15 20
39 gct aaa ttc cct gag tct gta ggt cat aag atc ctt tat ata agt acg 211
40 Ala Lys Phe Pro Glu Ser Val Gly His Lys Ile Leu Tyr Ile Ser Thr
41 25 30 35
43 caa tct aca cag cag gcc tta gca aca tat ctg gaa gct cta gat gcc 259
44 Gln Ser Thr Gln Gln Ala Leu Ala Thr Tyr Leu Glu Ala Leu Asp Ala
45 40 45 50
47 tac ggt gat cat gac ttc ttc gtt tta aga aaa atc gga gaa gac tat 307
48 Tyr Gly Asp His Asp Phe Phe Val Leu Arg Lys Ile Gly Glu Asp Tyr
49 55 60 65
51 ctc aag caa agc atc cac tcc tca gat ccg caa act aga aaa agc acc 355
52 Leu Lys Gln Ser Ile His Ser Ser Asp Pro Gln Thr Arg Lys Ser Thr
53 70 75 80 85
55 atc att gga gca ggc ctg gcg gga tct tca gaa gcc ttg gac gtg ctc 403
56 Ile Ile Gly Ala Gly Leu Ala Gly Ser Ser Glu Ala Leu Asp Val Leu
57 90 95 100
59 tcc caa gct atg gaa act gca gac ccc ctg cag cag cta ctg gtt tta 451
60 Ser Gln Ala Met Glu Thr Ala Asp Pro Leu Gln Gln Leu Leu Val Leu
61 105 110 115
63 tcg gca gtc tca gga cat ctt ggg aaa act tct gac gac tta ctg ttt 499

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64 Ser Ala Val Ser Gly His Leu Gly Lys Thr Ser Asp Asp Leu Leu Phe
65      120      125      130
67 aaa gct tta gca tct ccc tat cct gtc atc cgc tta gaa gcc gcc tat 547
68 Lys Ala Leu Ala Ser Pro Tyr Pro Val Ile Arg Leu Glu Ala Ala Tyr
69      135      140      145
71 aga ctt gct aat ttg aag aac act aaa gtc att gat cat cta cat tct 595
72 Arg Leu Ala Asn Leu Lys Asn Thr Lys Val Ile Asp His Leu His Ser
73 150      155      160      165
75 ttc att cat aag ctt ccc gaa gaa atc caa tgc cta tct gcg gca ata 643
76 Phe Ile His Lys Leu Pro Glu Glu Ile Gln Cys Leu Ser Ala Ala Ile
77      170      175      180
79 ttc cta cgc ttg gag act gaa gaa tct gat gct tat att cgg gat ctc 691
80 Phe Leu Arg Leu Glu Thr Glu Glu Ser Asp Ala Tyr Ile Arg Asp Leu
81      185      190      195
83 tta gct gcc aag aaa agc gcg att cgg agt gcc aca gct ttg cag atc 739
84 Leu Ala Ala Lys Lys Ser Ala Ile Arg Ser Ala Thr Ala Leu Gln Ile
85      200      205      210
87 gga gaa tac caa caa aaa cgc ttt ctt ccg aca ctt agg aat ttg cta 787
88 Gly Glu Tyr Gln Gln Lys Arg Phe Leu Pro Thr Leu Arg Asn Leu Leu
89      215      220      225
91 acg agt gcg tct cct caa gat caa gaa gct att ctt tat gct tta ggg 835
92 Thr Ser Ala Ser Pro Gln Asp Gln Glu Ala Ile Leu Tyr Ala Leu Gly
93 230      235      240      245
95 aag ctt aag gat ggt cag agc tac tac aat ata aaa aag caa ttg cag 883
96 Lys Leu Lys Asp Gly Gln Ser Tyr Tyr Asn Ile Lys Lys Gln Leu Gln
97      250      255      260
99 aag cct gat gtg gat gtc act tta gca gca gct caa gct tta att gct 931
100 Lys Pro Asp Val Asp Val Thr Leu Ala Ala Ala Gln Ala Leu Ile Ala
101      265      270      275
103 ttg ggg aaa gaa gag gac gct ctt ccc gtg ata aaa aag caa gca ctt 979
104 Leu Gly Lys Glu Glu Asp Ala Leu Pro Val Ile Lys Lys Gln Ala Leu
105      280      285      290
107 gag gag cgg cct cga gcc ctg tat gcc tta cgg cat cta ccc tct gag 1027
108 Glu Glu Arg Pro Arg Ala Leu Tyr Ala Leu Arg His Leu Pro Ser Glu
109      295      300      305
111 ata ggg att ccg att gcc ctg ccg ata ttc cta aaa act aag aac agc 1075
112 Ile Gly Ile Pro Ile Ala Leu Pro Ile Phe Leu Lys Thr Lys Asn Ser
113 310      315      320      325
115 gaa gcc aag ttg aat gta gct tta gct ctc tta gag tta ggg tgt gac 1123
116 Glu Ala Lys Leu Asn Val Ala Leu Ala Leu Leu Glu Leu Gly Cys Asp
117      330      335      340
119 acc cct aaa cta ctg gaa tac att acc gaa agg ctt gtc caa cca cat 1171
120 Thr Pro Lys Leu Leu Glu Tyr Ile Thr Glu Arg Leu Val Gln Pro His
121      345      350      355
123 tat aat gag act cta gcc ttg agt ttc tct aag ggg cgt act tta caa 1219
124 Tyr Asn Glu Thr Leu Ala Leu Ser Phe Ser Lys Gly Arg Thr Leu Gln
125      360      365      370
127 aat tgg aag cgg gtg aac atc ata gtc cct caa gat ccc cag gag agg 1267
128 Asn Trp Lys Arg Val Asn Ile Ile Val Pro Gln Asp Pro Gln Glu Arg

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131 gaa agg ttg ctc tcc aca acc cga ggt ctt gaa gag cag atc ctt acg 1315
132 Glu Arg Leu Leu Ser Thr Thr Arg Gly Leu Glu Glu Gln Ile Leu Thr
133 390      395      400      405
135 ttt ctc ttc cgc cta cct aaa gaa gct tac ctc ccc tgt att tat aag 1363
136 Phe Leu Phe Arg Leu Pro Lys Glu Ala Tyr Leu Pro Cys Ile Tyr Lys
137      410      415      420
139 ctt ttg gcg agt cag aaa act cag ctt gcc act act gcg att tct ttt 1411
140 Leu Leu Ala Ser Gln Lys Thr Gln Leu Ala Thr Thr Ala Ile Ser Phe
141      425      430      435
143 tta agt cac acc tca cat cag gaa gcc tta gat cta ctt ttc caa gct 1459
144 Leu Ser His Thr Ser His Gln Glu Ala Leu Asp Leu Leu Phe Gln Ala
145      440      445      450
147 gcg aag ctt cct gga gaa cct atc atc cgc gcc tat gca gat ctt gct 1507
148 Ala Lys Leu Pro Gly Glu Pro Ile Ile Arg Ala Tyr Ala Asp Leu Ala
149      455      460      465
151 att tat aat ctc acc aaa gat cct gaa aaa aaa cgt tct ctc cat gat 1555
152 Ile Tyr Asn Leu Thr Lys Asp Pro Glu Lys Lys Arg Ser Leu His Asp
153 470      475      480      485
155 tat gca aaa aag cta att cag gaa acc ttg tta ttt gtg gac acg gaa 1603
156 Tyr Ala Lys Lys Leu Ile Gln Glu Thr Leu Leu Phe Val Asp Thr Glu
157      490      495      500
159 aac caa aga ccc cat ccc agc atg ccc tat cta cgt tat cag gtc acc 1651
160 Asn Gln Arg Pro His Pro Ser Met Pro Tyr Leu Arg Tyr Gln Val Thr
161      505      510      515
163 cca gaa agc cgt acg aag ctc atg ttg gat att cta gag aca cta gcc 1699
164 Pro Glu Ser Arg Thr Lys Leu Met Leu Asp Ile Leu Glu Thr Leu Ala
165      520      525      530
167 acc tcg aag tct tcc gaa gat atc cgt tta ttg ata caa ctg atg acg 1747
168 Thr Ser Lys Ser Ser Glu Asp Ile Arg Leu Leu Ile Gln Leu Met Thr
169      535      540      545
171 gaa gga gat gca aaa aat ttc cca gtc ctt gca ggc tta ctc ata aaa 1795
172 Glu Gly Asp Ala Lys Asn Phe Pro Val Leu Ala Gly Leu Leu Ile Lys
173 550      555      560      565
175 att gtg gag taacccaac ctacgtctta tgaaacgttg cttcttattt 1844
176 Ile Val Glu
178 ctacgttccct ttgttcttat gggttcctca gctgatgctt tgactcatca agaggctgtg 1904
180 aaa 1907
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184 <211> LENGTH: 568
185 <212> TYPE: PRT
186 <213> ORGANISM: Chlamydia pneumoniae
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190 1 5 10 15
192 Pro Ile Ser Leu Val Ala Lys Phe Pro Glu Ser Val Gly His Lys Ile
193 20 25 30
195 Leu Tyr Ile Ser Thr Gln Ser Thr Gln Gln Ala Leu Ala Thr Tyr Leu
196 35 40 45

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198 Glu Ala Leu Asp Ala Tyr Gly Asp His Asp Phe Phe Val Leu Arg Lys
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201 Ile Gly Glu Asp Tyr Leu Lys Gln Ser Ile His Ser Ser Asp Pro Gln
202 65                      70                      75                      80
204 Thr Arg Lys Ser Thr Ile Ile Gly Ala Gly Leu Ala Gly Ser Ser Glu
205                      85                      90                      95
207 Ala Leu Asp Val Leu Ser Gln Ala Met Glu Thr Ala Asp Pro Leu Gln
208                      100                      105                      110
210 Gln Leu Leu Val Leu Ser Ala Val Ser Gly His Leu Gly Lys Thr Ser
211                      115                      120                      125
213 Asp Asp Leu Leu Phe Lys Ala Leu Ala Ser Pro Tyr Pro Val Ile Arg
214                      130                      135                      140
216 Leu Glu Ala Ala Tyr Arg Leu Ala Asn Leu Lys Asn Thr Lys Val Ile
217 145                      150                      155                      160
219 Asp His Leu His Ser Phe Ile His Lys Leu Pro Glu Glu Ile Gln Cys
220                      165                      170                      175
222 Leu Ser Ala Ala Ile Phe Leu Arg Leu Glu Thr Glu Glu Ser Asp Ala
223                      180                      185                      190
225 Tyr Ile Arg Asp Leu Leu Ala Ala Lys Lys Ser Ala Ile Arg Ser Ala
226                      195                      200                      205
228 Thr Ala Leu Gln Ile Gly Glu Tyr Gln Gln Lys Arg Phe Leu Pro Thr
229                      210                      215                      220
231 Leu Arg Asn Leu Leu Thr Ser Ala Ser Pro Gln Asp Gln Glu Ala Ile
232 225                      230                      235                      240
234 Leu Tyr Ala Leu Gly Lys Leu Lys Asp Gly Gln Ser Tyr Tyr Asn Ile
235                      245                      250                      255
237 Lys Lys Gln Leu Gln Lys Pro Asp Val Asp Val Thr Leu Ala Ala Ala
238                      260                      265                      270
240 Gln Ala Leu Ile Ala Leu Gly Lys Glu Glu Asp Ala Leu Pro Val Ile
241                      275                      280                      285
243 Lys Lys Gln Ala Leu Glu Glu Arg Pro Arg Ala Leu Tyr Ala Leu Arg
244                      290                      295                      300
246 His Leu Pro Ser Glu Ile Gly Ile Pro Ile Ala Leu Pro Ile Phe Leu
247 305                      310                      315                      320
249 Lys Thr Lys Asn Ser Glu Ala Lys Leu Asn Val Ala Leu Ala Leu Leu
250                      325                      330                      335
252 Glu Leu Gly Cys Asp Thr Pro Lys Leu Glu Tyr Ile Thr Glu Arg
253                      340                      345                      350
255 Leu Val Gln Pro His Tyr Asn Glu Thr Leu Ala Leu Ser Phe Ser Lys
256                      355                      360                      365
258 Gly Arg Thr Leu Gln Asn Trp Lys Arg Val Asn Ile Ile Val Pro Gln
259                      370                      375                      380
261 Asp Pro Gln Glu Arg Glu Arg Leu Leu Ser Thr Thr Arg Gly Leu Glu
262 385                      390                      395                      400
264 Glu Gln Ile Leu Thr Phe Leu Phe Arg Leu Pro Lys Glu Ala Tyr Leu
265                      405                      410                      415
267 Pro Cys Ile Tyr Lys Leu Leu Ala Ser Gln Lys Thr Gln Leu Ala Thr
268                      420                      425                      430
270 Thr Ala Ile Ser Phe Leu Ser His Thr Ser His Gln Glu Ala Leu Asp

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271          435          440          445
273 Leu Leu Phe Gln Ala Ala Lys Leu Pro Gly Glu Pro Ile Ile Arg Ala
274          450          455          460
276 Tyr Ala Asp Leu Ala Ile Tyr Asn Leu Thr Lys Asp Pro Glu Lys Lys
277 465          470          475          480
279 Arg Ser Leu His Asp Tyr Ala Lys Lys Leu Ile Gln Glu Thr Leu Leu
280          485          490          495
282 Phe Val Asp Thr Glu Asn Gln Arg Pro His Pro Ser Met Pro Tyr Leu
283          500          505          510
285 Arg Tyr Gln Val Thr Pro Glu Ser Arg Thr Lys Leu Met Leu Asp Ile
286          515          520          525
288 Leu Glu Thr Leu Ala Thr Ser Lys Ser Ser Glu Asp Ile Arg Leu Leu
289          530          535          540
291 Ile Gln Leu Met Thr Glu Gly Asp Ala Lys Asn Phe Pro Val Leu Ala
292 545          550          555          560
294 Gly Leu Leu Ile Lys Ile Val Glu
295          565
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299 <211> LENGTH: 44
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: 5' PCR primer
306 <400> SEQUENCE: 3
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314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: 3' PCR primer
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/662,812

DATE: 05/09/2002

TIME: 13:44:42

Input Set : A:\seqed.app.txt

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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date